

```

DB 1 MHKAGLLGICARAMNSVRRASGSMTRRDPPLANKVALYASTDGIQFALARRLAODGAHV 60
QY 61 VSSKROONVDOAVATLQEGSLVGTGCHVGAKADERRLVATVAVLHGGIDILVSNAAVN 120
DB 61 VSSKROONVDOAVATLQEGSLVGTGCHVGAKADERRLVATVAVLHGGIDILVSNAAVN 120
QY 121 PFFGSINDVTEEVWMDKTDINVKAPALMTKAVPEMERKGGGSVIVSSIAAFSPGFS 180
DB 121 PFFGSINDVTEEVWMDKTDINVKAPALMTKAVPEMERKGGGSVIVSSIAAFSPGFS 180
QY 181 PYNVSKTALLGLTKTIAELAPRNIRVNCIAPGLIKTSFRMLMDKKEESMKTLLRIR 240
DB 181 PYNVSKTALLGLTKTIAELAPRNIRVNCIAPGLIKTSFRMLMDKKEESMKTLLRIR 240
QY 241 RLGEPEDCAGIVSFLCSEDSASTTGEIVVVGGSIPSSL 278
DB 241 RLGEPEDCAGIVSFLCSEDSASTTGEIVVVGGSIPSSL 278

RESULT 3
AAB93414
ID AAB93414 standard; Protein: 278 AA.
AC AAB93414;
DE 26-JUN-2001 (first entry)
XX
XX Human protein sequence SEQ ID NO:12620.
XX
XX Homo sapiens.
XX
XX EPI074617-A2.
XX
XX 07-FEB-2001.
XX
XX 28-JUL-2000; 2000EP-0116126.
XX
XX 29-JUL-1999; 99TP-0248036.
XX
XX 27-AUG-1999; 99UP-0300233.
XX
XX 11-JAN-2000; 2000JP-0118776.
XX
XX 02-MAY-2000; 2000JP-0118767.
XX
XX 09-JUN-2000; 2000JP-0241899.
XX
XX (HELI-) HELIX RES INST.
XX
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
XX Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602
XX full-length cDNAs defined in the specification, and for the detection
XX and/or diagnosis of the abnormality of the proteins encoded by the
XX full-length cDNAs -
XX
XX Claim 8; SEQ ID 12620; 2537bp + CD ROM; English.
XX
XX The present invention describes primer sets for synthesizing 5602
XX full-length cDNAs defined in the specification. Where a primer set
XX comprises: (a) an oligo-dT primer and an oligonucleotide complementary
XX to the complementary strand of a polynucleotide which comprises one of
XX the 5602 nucleotide sequences defined in the specification, where the
XX oligonucleotide comprises at least 15 nucleotides; or (b) a combination
XX of an oligonucleotide comprising a sequence complementary to the
XX complementary strand of a polynucleotide which comprises a 5'-end
XX sequence and an oligonucleotide comprising a sequence complementary to a
XX polynucleotide which comprises a 3'-end sequence, where the
XX oligonucleotide comprises at least 15 nucleotides and the combination of
XX the 5'-end sequence/3'-end sequence is selected from those defined in
XX the specification. The primer sets can be used in antisense therapy and

```

```

CC in gene therapy. The primers are useful for synthesizing polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AA992445 to
CC AA995893 represent human amino acid sequences; and AAH13629 to AAH13632
CC represent oligonucleotides, all of which are used in the exemplification
CC of the present invention.
XX
XX Sequence 278 AA:
SQ
XX
XX Query Match 99.7%; Score 1395; DB 22; Length 278;
XX Best Local Similarity 99.6%; Pred. No. 2e-131;
XX Matches 277; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MHKAGLLGICARAMNSVRRASGSMTRRDPPLANKVALYASTDGIQFALARRLAODGAHV 60
DB 1 MHKAGLLGICARAMNSVRRASGSMTRRDPPLANKVALYASTDGIQFALARRLAODGAHV 60
QY 61 VSSKROONVDOAVATLQEGSLVGTGCHVGAKADERRLVATVAVLHGGIDILVSNAAVN 120
DB 61 VSSKROONVDOAVATLQEGSLVGTGCHVGAKADERRLVATVAVLHGGIDILVSNAAVN 120
QY 121 PFFGSINDVTEEVWMDKTDINVKAPALMTKAVPEMERKGGGSVIVSSIAAFSPGFS 180
DB 121 PFFGSINDVTEEVWMDKTDINVKAPALMTKAVPEMERKGGGSVIVSSIAAFSPGFS 180
QY 181 PYNVSKTALLGLTKTIAELAPRNIRVNCIAPGLIKTSFRMLMDKKEESMKTLLRIR 240
DB 181 PYNVSKTALLGLTKTIAELAPRNIRVNCIAPGLIKTSFRMLMDKKEESMKTLLRIR 240
QY 241 RLGEPEDCAGIVSFLCSEDSASTTGEIVVVGGSIPSSL 278
DB 241 RLGEPEDCAGIVSFLCSEDSASTTGEIVVVGGSIPSSL 278

RESULT 4
AAY68735
ID AAY68735 standard; Protein: 278 AA.
AC AAY68735;
DE 05-MAY-2000 (first entry)
XX
XX Short chain alcohol dehydrogenase-related molecule SCRM-1 protein.
XX
XX Human; short chain alcohol dehydrogenase-related molecule;
XX SCAD-related molecule; SCRM-1; SCRM-2; metabolic regulator;
XX cell proliferation regulator; inflammation regulator;
XX cell proliferative disorder; immune disorder; arteriosclerosis;
XX atherosclerosis; bursitis; cirrhosis; hepatitis; AIDS;
XX Addison's disease; adult respiratory distress syndrome; allergy;
XX ankylosing spondylitis; amyloidosis; cancer.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Modified-site 16
XX /note= "potential protein kinase C phosphorylation site"
XX Modified-site 21
XX /note= "potential protein kinase C phosphorylation site"
XX Modified-site 25
XX /note= "potential casein kinase II phosphorylation site
XX and potential protein kinase C phosphorylation
XX site"
XX Modified-site 31
XX /note= "potential protein kinase C phosphorylation site"
XX Region 33..45
XX /note= "SCAD motif"
XX Region 34..51
XX /note= "glucose/ribitol dehydrogenase motif"
XX Binding-site 39..46

```

FT Modified-site /note= "AMP-binding domain"  
 FT 62  
 FT /note= "potential protein kinase C phosphorylation site"  
 FT Modified-site 63  
 FT /note= "potential protein kinase C phosphorylation site"  
 FT Region 108..119  
 FT /note= "glucose/ribitol dehydrogenase motif"  
 FT Region 108..118  
 FT /note= "SCAD motif"  
 FT Region 108..119  
 FT /note= "SCAD motif"  
 FT Modified-site 125  
 FT /note= "potential casein kinase II phosphorylation site"  
 FT Region 156..172  
 FT /note= "glucose/ribitol dehydrogenase motif"  
 FT Region 162..199  
 FT /note= "SCAD motif"  
 FT Region 162..213  
 FT /note= "SCAD signature sequence"  
 FT Region 169..197  
 FT /note= "SCAD family signature sequence"  
 FT Region 182..201  
 FT /note= "glucose/ribitol dehydrogenase motif"  
 FT Domain 182..186  
 FT /note= "canonical catalytic site of SCADS"  
 FT Region 203..220  
 FT /note= "glucose/ribitol dehydrogenase motif"  
 FT Region 204..213  
 FT /note= "SCAD motif"  
 FT Modified-site 232  
 FT /note= "potential casein kinase II phosphorylation site  
 FT and potential protein kinase C phosphorylation  
 FT site"  
 FT Modified-site 236  
 FT /note= "potential protein kinase C phosphorylation site"  
 FT Region 238..258  
 FT /note= "glucose/ribitol dehydrogenase motif"  
 FT  
 PN WO200004135-A2.  
 PD 27-JAN-2000.  
 XX  
 PF 16-JUL-1999; 99WO-US16164.  
 XX  
 PR 16-JUL-1998; 98US-0116750.  
 PR 16-JUL-1998; 98US-0160074.  
 XX  
 PA (INCYTE) INCYTE PHARM INC.  
 PI Bandman O, Tang YT, Corley NC, Azimzai Y, Baughn MR;  
 XX WPI: 2000-171266/15.  
 DR N-PSDB; AAZ46080.  
 XX  
 PT New short chain alcohol dehydrogenase polypeptides useful for  
 PT diagnosis, treatment and prevention of cell proliferative disorders  
 PT such as atherosclerosis, cirrhosis and cancers of various tissues  
 XX  
 PS Claim 1, Fig 1A-D, 78pp; English.  
 CC  
 CC The present sequence represents a human short chain alcohol dehydrogenase  
 CC (SCAD)-related molecule designated SCRM-1. The specification also  
 CC describes SCRM-2. SCRM proteins are metabolic, cell proliferation and  
 CC inflammation regulators. The SCRM polynucleotides and polypeptides are  
 CC used for treating or preventing a cell proliferative or immune disorder  
 CC in humans. Cell proliferative disorders include arteriosclerosis,  
 CC atherosclerosis, bursitis, cirrhosis, and hepatitis. Immune disorders  
 CC include AIDS, Addison's disease, adult respiratory distress syndrome,  
 CC allergies, ankylosing spondylitis, and amyloidosis. The vectors,  
 CC agonists, antagonists, antibodies and complementary sequences are also  
 CC used for treating the above conditions. The polynucleotides and  
 CC polypeptides are also used for treating cancers of various tissues  
 CC such as adrenal gland, bladder, bone, bone marrow, and brain.

XX Sequence 278 AA:  
 SQ  
 Query Match 94.9%; Score 1327; DB 21; Length 278;  
 Best Local Similarity 96.4%; Pred. No. 1.3e-124;  
 Matches 268; Conservative 0; Mismatches 10; Indels 0; Gaps 0;  
 QY 1 MHKAGLGLCARPNSVYRMASGATRRDPLANKYALVTASTDGIHAIARLRACDGAHV 60  
 DB 1 MHMARRLGLCARPNSVYRMASGATRRDPLANKYALVTASTDGIHAIARLRACDGAHV 60  
 QY 61 VSSRQONVDOAVATLQGGSLVTVGVCHVAKADRRRLVAVKIHGIDILVSNAAVN 120  
 DB 61 VSSRQONVDOAVATLQGGSLVTVGVCHVAKADRRRLVAVKIHGIDILVSNAAVN 120  
 QY 121 PFGSGINDVTEFWYDKTLDINKAPALMTKAVYEMKRGGSVTVSSIAFSPSPGS 180  
 DB 121 PFGSGINDVTEFWYDKTLDINKAPALMTKAVYEMKRGGSVTVSSIAFSPSPGS 180  
 QY 181 PYNVSKTALLGLAKTALIELAPRNIRVNCIAPGLIKTSFRMLMDKKEESMKETLRIR 240  
 DB 181 PYNVSKTALLGLAKTALIELAPRNIRVNCIAPGLIKTSFRMLMDKKEESMKETLRIR 240  
 QY 241 RLGEPEDCAGIVSEFLCSEDASTYTGFTVVGGSPTSL 278  
 DB 241 RLGEPEDCAGIVSEFLCSEDASTYTGFTVVGGSPTSL 278  
 RESULT 5  
 AAU30722  
 ID AAU30722 standard; Protein; 477 AA.  
 AC AAU30722;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Novel human secreted protein #1213.  
 XX  
 KW Human; vaccination; gene therapy; nutritional supplement;  
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;  
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.  
 OS Homo sapiens.  
 PN WO200179449-A2.  
 PD 25-OCT-2001.  
 XX  
 PF 16-APR-2001; 2001WO-US08656.  
 XX  
 PR 18-APR-2000; 2000US-0552929.  
 PR 26-JAN-2001; 2001US-0770160.  
 XX  
 PA (HYSEQ-) HYSEQ INC.  
 PI Tang YT, Liu C, Dimanac RT;  
 XX WPI: 2001-611725/70.  
 DR  
 PT Nucleic acids encoding a range of human polypeptides, useful in genetic  
 PT vaccination, testing and therapy -  
 XX  
 PS Claim 20; Page 336; 765pp; English.  
 CC  
 CC The invention relates to novel human secreted polypeptides. The  
 CC polypeptides and antibodies to the polypeptides are useful for  
 CC determining the presence of or predisposition to a disease associated  
 CC with altered levels of polypeptide. The polypeptides are also useful for  
 CC identifying agents (agonists and antagonists) that bind to them. Cells  
 CC expressing the proteins are useful for identifying a therapeutic agent  
 CC for use in treatment of a pathology related to aberrant expression or  
 CC physiological interactions of the polypeptide. Vectors comprising  
 CC the nucleic acids encoding the polypeptides and cells genetically